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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: NAGATA, Shigekazu  
ITOH, Naoto  
YONEHARA, Shin

(ii) TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
ANTIGEN

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
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(D) STATE: VA  
(E) COUNTRY: USA  
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/468,560  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MURPHY JR., GERALD M.  
(B) REGISTRATION NUMBER: 28,977  
(C) REFERENCE/DOCKET NUMBER: 20-4393P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 703-205-8000  
(B) TELEFAX: 703-205-8050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2534 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 195..1202

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 195..242

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 243..1199

(ix) FEATURE:

(A) NAME/KEY: polyA\_site  
(B) LOCATION: 1831..1836

(ix) FEATURE:

(A) NAME/KEY: polyA\_site  
(B) LOCATION: 2352..2357

(ix) FEATURE:

(A) NAME/KEY: polyA\_site  
(B) LOCATION: 2518..2532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACGCTTCTG	GGGAGTGAGG	GAAGCGGTTT	ACGAGTGACT	TGGCTGGAGC	CTCAGGGGCG	60										
GGCACTGGCA	CGGAAACACAC	CCTGAGGCCA	GCCCTGGCTG	CCCAGCCGGGA	GCTGCCCTCTT	120										
CTCCCGCGGG	TTGGTGGACC	CGCTCAGTAC	GGAGTTGGGG	AAGCTCTTTC	ACTTCGGAGG	180										
ATTGCTAAC	AACC	ATG CTG	GGC ATC	TGG ACC	CTC CTA	CCT CTG	GTT CTT	230								
Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	-5				
-16	-15					-10										
ACG	TCT	GCT	AGA	TTA	TCG	TCC	AAA	AGT	GTT	AAT	GCC	CAA	GTG	ACT	278	
Thr	Ser	Val	Ala	Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	
1						5								10		
GAC	ATC	AAC	TCC	AAG	GGA	TTG	GAA	TTG	AGG	AAG	ACT	GTT	ACT	ACA	GTT	326
Asp	Ile	Asn	Ser	Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	
15						20						25				
GAG	ACT	CAG	AAC	TTG	GAA	GGC	CTG	CAT	CAT	GAT	GGC	CAA	TTC	TGC	CAT	374
Glu	Thr	Gln	Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	
30						35						40				
AAG	CCC	TGT	CCT	CCA	GGT	GAA	AGG	AAA	GCT	AGG	GAC	TGC	ACA	GTC	AAT	422
Lys	Pro	Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	
45						50				55		60				
GGG	GAT	GAA	CCA	GAC	TGC	GTG	CCC	TGC	CAA	GAA	GGG	AAG	GAG	TAC	ACA	470
Gly	Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	
65						70						75				
GAC	AAA	GCC	CAT	TTT	TCT	TCC	AAA	TGC	AGA	AGA	TGT	AGA	TTG	TGT	GAT	518
Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	Asp	
80							85					90				
GAA	GGA	CAT	GGC	TTA	GAA	GTG	GAA	ATA	AAC	TGC	ACC	CGG	ACC	CAG	AAT	566
Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr	Gln	Asn	
95						100						105				
ACC	AAG	TGC	AGA	TGT	AAA	CCA	AAC	TTT	TTT	TGT	AAC	TCT	ACT	GTA	TGT	614

Thr Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys  
 110 115 120

GAA CAC TGT GAC CCT TGC ACC AAA TGT GAA CAT GGA ATC ATC AAG GAA 662  
 Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu  
 125 130 135 140

TGC ACA CTC ACC AGC AAC ACC AAG TGC AAA GAG GAA GGA TCC AGA TCT 710  
 Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser  
 145 150 155

AAC TTG GGG TGG CTT TGT CTT CTT TTG CCA ATT CCA CTA ATT GTT 758  
 Asn Leu Gly Trp Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val  
 160 165 170

TGG CTG AAC AGA AAA GAA CTA CAG AAA ACA TGC AGA AAA CAC AGA AAA 806  
 Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys  
 175 180 185

GAA AAC CAA GGT TCT CAT GAA TCT CCA ACC TTA AAT CCT GAA ACA GTG 854  
 Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val  
 190 195 200

GCA ATA AAT TTA TCT GAT GTT GAC TTG AGT AAA TAT ATC ACC ACT ATT 902  
 Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile  
 205 210 215 220

GCT GGA GTC ATG ACA CTA AGT CAA GTT AAA GGC TTT GTT CGA AAG AAT 950  
 Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn  
 225 230 235

GGT GTC AAT GAA GCC AAA ATA GAT GAG ATC AAG AAT GAC AAT GTC CAA 998  
 Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln  
 240 245 250

GAC ACA GCA GAA CAG AAA GTT CAA CTG CTT CGT AAT TGG CAT CAA CTT 1046  
 Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu  
 255 260 265

CAT GGA AAA GAA GCG TAT GAC ACA TTG ATT AAA CAT CTC AAA AAA 1094  
 His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys  
 270 275 280

GCC AAA CTT TGT ACT CTT GCA GAG AAA ATT CAG ACT ATC ATC CTC AAA 1142  
 Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys  
 285 290 295 300

GAC ATT ACT AGT GAC TCA GAA AAT TCA AAC TTC AGA AAT GAA ATC CAA 1190  
 Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln  
 305 310 315

AGC TTG GTC TAG AGTGAAAAAC AACAAATTCA GTTCTGAGTA TATGCAATTA 1242  
 Ser Leu Val

GTGTTGAAA AGATTCTTAA TAGCTGGCTG TAAATACTGC TTGGTTTTT ACTGGGTACA 1302

TTTTATCATT TATTAGCGCT GAAGAGCCAA CATATTTGTA GATTTTAAT ATCTCATGAT 1362

TCTGCCTCCA AGGATGTTA AAATCTAGTT GGGAAAACAA ACTTCATCAA GAGTAAATGC 1422

AGTGGCATGC TAAGTACCCA AATAGGAGTG TATGCAGAGG ATGAAAGATT AAGATTATGC 1482  
 TCTGGCATCT AACATATGAT TCTGTAGTAT GAATGTAATC AGTGTATGTT AGTACAAATG 1542  
 TCTATCCACA GGCTAACCCC ACTCTATGAA TCAATAGAAG AAGCTATGAC CTTTGCTGA 1602  
 ATATCAGTT ACTGAAACAGG CAGGCCACTT TCCCTCTAAA TTACCTCTGA TAACTCTAGA 1662  
 GATTTACCA TATTTCTAAA CTTTGTAT TAACTCTGAGA AGATCATATT TATGTAAAGT 1722  
 ATATGTATT GAGTGCAGAA TTTAAATAAG GCTCTACCTC AAAGACCTT GCACAGTTA 1782  
 TTGGTGTCA ATTATACAAT ATTTCAATTG TGAATTACACA TAGAAAACAT TAAATTATAA 1842  
 TGTTTGACTA TTATATATGT GTATGCATT TACTGGCTCA AACTACCTA CTTCTTCTC 1902  
 AGGCATCAAA AGCATTTGA GCAGGAGAGT ATTACTAGAG CTTGCCACC TCTCCATT 1962  
 TGCCTGGTG CTCATCTAA TGGCCTAATG CACCCCCAAA CATGGAAATA TCACCAAAA 2022  
 ATACTTAATA GTCCACCAAA AGGCAAGACT GCCCTTAGAA ATTCTAGCCT GGTTGGAGA 2082  
 TACTAACTGC TCTCAGAGAA AGTAGCTTG TGACATGTCA TGAACCCATG TTTGCAATCA 2142  
 AAGATGATAA AATAGATTCT TATTTTCCC CCACCCCCGA AAATGTCAA TAATGTCCC 2202  
 TGTAAAACCT GCTACAAATG GCAGCTTATA CATAGCAATG GTAAAATCAT CATCTGGATT 2262  
 TAGGAATTGC TCTTGTCA CCCTCAAGTT TCTAAGATT AAGATTCTCC TTACTACTAT 2322  
 CCTACGTTA AATATCTTG AAAGTTGTA TAAATGTGA ATTTAAGAA ATAATATTAA 2382  
 TATTTCTGTA AATGTAACGT GTGAAGATAG TTATAAACTG AAGCAGATAC CTGGAACCAC 2442  
 CTAAAGAACT TCCATTTATG GAGGATTTT TTGCCCTTG TGTTGGAAT TATAAAATAT 2502  
 AGGTAAAAGT ACGTAATTAA ATAATGTTT TG 2534

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
 -16 -15 -10 -5

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
 1 5 10 15

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Val Glu Thr Gln Asn  
 20 25 30

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 35 40 45

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 50 55 60  
 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 65 70 75 80  
 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
 85 90 95  
 Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
 100 105 110  
 Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
 115 120 125  
 Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr  
 130 135 140  
 Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp  
 145 150 155 160  
 Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg  
 165 170 175  
 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly  
 180 185 190  
 Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu  
 195 200 205  
 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met  
 210 215 220  
 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu  
 225 230 235 240  
 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu  
 245 250 255  
 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys  
 260 265 270  
 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys  
 275 280 285  
 Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser  
 290 295 300  
 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro  
1 5 10 15

Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp  
20 25 30

Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys  
35 40 45

Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly  
50 55 60

His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys  
65 70 75 80

Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His  
85 90 95

Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr  
100 105 110

Leu Thr Ser Asn Thr Lys Cys  
115

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i.i) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys  
1 5 10 15

Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly  
20 25 30

Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr  
35 40 45

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg  
50 55 60

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp  
65 70 75 80

Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu
85									90				95		
Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val
	100							105				110			
His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala
	115						120				125				
Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys
	130				135					140					
Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys							
	145					150									

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 163 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys
1					5				10				15		
Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	Thr	Lys	Thr
	20								25				30		
Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr	Gln	Leu
	35						40					45			
Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Asp
	50				55				60						
Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys
	65				70				75			80			
Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys
					85				90			95			
Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala
			100				105				110				
Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro
	115					120				125					
Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His
	130					135				140					
Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala
	145					150				155			160		
Val	Cys	Thr													

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala  
1 5 10 15

Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr  
20 25 30

Val Cys Glu Pro Cys Leu Asp Ser Val Thr Ser Ser Asp Val Val Ser  
35 40 45

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser  
50 55 60

Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala  
65 70 75 80

Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg  
85 90 95

Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln  
100 105 110

Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala  
115 120 125

Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu  
130 135 140

Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser Leu  
 1 5 10 15

Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu  
 20 25 30

Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn  
 35 40 45

Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly  
 50 55 60

Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr  
 65 70 75 80

Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val  
 85 90 95

Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr  
 100 105 110

Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser  
 115 120 125

Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Thr Ser Cys Glu Thr  
 130 135 140

Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn Lys Thr Asp Val Val  
 145 150 155 160

Cys Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys Cys Cys Arg Glu  
 1 5 10 15

Cys Gln Pro Gly His Gly Met Val Ser Arg Cys Asp His Thr Arg Asp  
 20 25 30

Thr Val Cys His Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys  
 35 40 45

Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg Cys Asp  
 50 55 60

His Thr Arg Asp Thr Val Cys His Cys Arg Pro Gly Thr Gln Pro Arg  
 65 70 75 80  
 Gln Asp Ser Ser His Lys Phe Gly Val Asp Cys Val Pro Cys Pro Pro  
 85 90 95  
 Gly His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn  
 100 105 110  
 Cys Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu  
 115 120 125  
 Asp Thr Val Cys Glu  
 130

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp  
 1 5 10 15  
 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His  
 20 25 30  
 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp  
 1 5 10 15  
 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His  
 20 25 30  
 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp  
1 5 10 15

Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His  
20 25 30

Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser  
35 40 45

REF ID: A65912